

SEQUENCE LISTING

<110> INCYTE PHARMACEUTICALS, INC.
 BANDMAN, Olga
 TANG, Y. Tom
 CORLEY, Neil C.
 AZIMZAI, Yalda
 BAUGHN, Mariah R.

<120> SCAD-RELATED MOLECULES

<130> PF-0559 PCT

<140> To Be Assigned

<141> Herewith

<150> 09/116,750; Unassigned

<151> 1998-07-16; 1998-07-16

<160> 6

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 278

<212> PRT

<213> HOMO SAPIENS

<220>

<221> misc_feature

<223> Incyte Clone No: 1240869

<300>

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			20					25					30		
Lys	Val	Ala	Leu	Val	Thr	Ala	Ser	Thr	Asp	Gly	Ile	Gly	Phe	Ala	Ile
		35					40					45			
Ala	Arg	Arg	Leu	Ala	Gln	Asp	Arg	Ala	His	Val	Val	Val	Ser	Ser	Arg
		50			55					60					
Lys	Gln	Gln	Asn	Val	Asp	Gln	Ala	Val	Ala	Thr	Leu	Gln	Gly	Glu	Gly
65			70						75					80	
Leu	Ser	Val	Thr	Gly	Thr	Val	Cys	His	Val	Gly	Lys	Ala	Glu	Asp	Arg
			85					90						95	
Glu	Arg	Leu	Val	Ala	Thr	Ala	Val	Lys	Leu	His	Gly	Gly	Ile	Asp	Ile
			100					105					110		
Leu	Val	Ser	Asn	Ala	Ala	Val	Asn	Pro	Phe	Phe	Gly	Ser	Ile	Met	Asp
		115				120						125			
Val	Thr	Glu	Glu	Val	Trp	Asp	Lys	Thr	Leu	Asp	Ile	Asn	Val	Lys	Ala
	130				135					140					
Pro	Ala	Leu	Met	Thr	Lys	Ala	Val	Val	Pro	Glu	Met	Glu	Lys	Arg	Gly
145				150				155						160	
Gly	Gly	Ser	Val	Val	Ile	Val	Ser	Ser	Ile	Ala	Ala	Phe	Ser	Pro	Ser
			165				170							175	
Pro	Gly	Phe	Ser	Pro	Tyr	Asn	Val	Ser	Lys	Thr	Ala	Leu	Leu	Gly	Leu
		180					185					190			
Asn	Asn	Thr	Leu	Ala	Ile	Glu	Leu	Ala	Pro	Arg	Asn	Ile	Arg	Val	Asn
	195					200					205				
Cys	Leu	Ala	Pro	Gly	Leu	Ile	Lys	Thr	Ser	Phe	Ser	Arg	Met	Leu	Trp
	210				215						220				

Met Asp Lys Glu Lys Glu Glu Ser Met Lys Glu Thr Leu Arg Ile Arg
 225 230 235 240
 Arg Leu Gly Glu Pro Glu Asp Cys Ala Gly Ile Val Ser Phe Leu Cys
 245 250 255
 Ser Glu Asp Ala Ser Tyr Ile Thr Gly Glu Thr Val Val Val Gly Gly
 260 265 270
 Gly Thr Pro Ser Arg Leu
 275

<210> 2

<211> 564

<212> PRT

<213> HOMO SAPIENS

<220>

<221> misc_feature

<223> Incyte Clone No: 2060002

<300>

<400> 2

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 Tyr Ala Tyr Pro Ser Asp Tyr Asp Met His Thr Gly Asp Pro Lys Gln
 20 25 30
 Asp Leu Ala Tyr Glu Arg Gln Tyr Glu Gln Gln Thr Tyr Gln Val Ile
 35 40 45
 Pro Glu Val Ile Lys Asn Phe Ile Gln Tyr Phe His Lys Thr Val Ser
 50 55 60
 Asp Leu Ile Asp Gln Lys Val Tyr Glu Leu Gln Ala Ser Arg Val Ser
 65 70 75 80
 Ser Asp Val Ile Asp Gln Lys Val Tyr Glu Ile Gln Asp Ile Tyr Glu
 85 90 95
 Asn Ser Trp Thr Lys Leu Thr Glu Arg Phe Phe Lys Asn Thr Pro Trp
 100 105 110
 Pro Glu Ala Glu Ala Ile Ala Pro Gln Val Gly Asn Asp Ala Val Phe
 115 120 125
 Leu Ile Leu Tyr Lys Glu Leu Tyr Tyr Arg His Ile Tyr Ala Lys Val
 130 135 140
 Ser Gly Gly Pro Ser Leu Glu Gln Arg Phe Glu Ser Tyr Tyr Asn Tyr
 145 150 155 160
 Cys Asn Leu Phe Asn Tyr Ile Leu Asn Ala Asp Gly Pro Ala Pro Leu
 165 170 175
 Glu Leu Pro Asn Gln Trp Leu Trp Asp Ile Ile Asp Glu Phe Ile Tyr
 180 185 190
 Gln Phe Gln Ser Phe Ser Gln Tyr Arg Cys Lys Thr Ala Lys Lys Ser
 195 200 205
 Glu Glu Glu Ile Asp Phe Leu Arg Ser Asn Pro Lys Ile Trp Asn Val
 210 215 220
 His Ser Val Leu Asn Val Leu His Ser Leu Val Asp Lys Ser Asn Ile
 225 230 235 240
 Asn Arg Gln Leu Glu Val Tyr Thr Ser Gly Gly Asp Pro Glu Ser Val
 245 250 255
 Ala Gly Glu Tyr Gly Arg His Ser Leu Tyr Lys Met Leu Gly Tyr Phe
 260 265 270
 Ser Leu Val Gly Leu Leu Arg Leu His Ser Leu Leu Gly Asp Tyr Tyr
 275 280 285
 Gln Ala Ile Lys Val Leu Glu Asn Ile Glu Leu Asn Lys Lys Ser Met
 290 295 300
 Tyr Ser Arg Val Pro Glu Cys Gln Val Thr Thr Tyr Tyr Tyr Val Gly
 305 310 315 320
 Phe Ala Tyr Leu Met Met Arg Arg Tyr Gln Asp Ala Ile Arg Val Phe
 325 330 335
 Ala Asn Ile Leu Leu Tyr Ile Gln Arg Thr Lys Ser Met Phe Gln Arg
 340 345 350

Thr Thr Tyr Lys Tyr Glu Met Ile Asn Lys Gln Asn Glu Gln Met His
 355 360 365
 Ala Leu Leu Ala Ile Ala Leu Thr Met Tyr Pro Met Arg Ile Asp Glu
 370 375 380
 Ser Ile His Leu Gln Leu Arg Glu Lys Tyr Gly Asp Lys Met Leu Arg
 385 390 395 400
 Met Gln Lys Gly Asp Pro Gln Val Tyr Glu Glu Leu Phe Ser Tyr Ser
 405 410 415
 Cys Pro Lys Phe Leu Ser Pro Val Val Pro Asn Tyr Asp Asn Val His
 420 425 430
 Pro Asn Tyr His Lys Glu Pro Phe Leu Gln Gln Leu Lys Val Phe Ser
 435 440 445
 Asp Glu Val Gln Gln Gln Ala Gln Leu Ser Thr Ile Arg Ser Phe Leu
 450 455 460
 Lys Leu Tyr Thr Thr Met Pro Val Ala Lys Leu Ala Gly Phe Leu Asp
 465 470 475 480
 Leu Thr Glu Gln Glu Phe Arg Ile Gln Leu Leu Val Phe Lys His Lys
 485 490 495
 Met Lys Asn Leu Val Trp Thr Ser Gly Ile Ser Ala Leu Asp Gly Glu
 500 505 510
 Phe Gln Ser Ala Ser Glu Val Asp Phe Tyr Ile Asp Lys Asp Met Ile
 515 520 525
 His Ile Ala Asp Thr Lys Val Ala Arg Arg Tyr Gly Asp Phe Phe Ile
 530 535 540
 Arg Gln Ile His Lys Phe Glu Glu Leu Asn Arg Thr Leu Lys Lys Met
 545 550 555 560
 Gly Gln Arg Pro

<210> 3
 <211> 1280
 <212> DNA
 <213> HOMO SAPIENS

<220>
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 <223> Incyte Clone No: 1240869

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 acaaataagg tggccctggt aacggcctcc accgacggga tcggcttcgc catcgcccg 180
 cgtttggccc aggacagggc ccacgtgggtc gtcagcagcc ggaagcagca gaatgtggac 240
 caggcgggtg ccacgctgca gggggagggg ctgagcgtga cgggcaccgt gtgccatgtg 300
 ggggaaggcgg aggaccggga gcggctgggt gccacggctg tgaagcttca tggaggtatc 360
 gatatacctag tctccaatgc tgctgtcaac cttttctttg gaagcataat ggatgtcact 420
 gaggaggtgt gggacaagac tctggacatt aatgtgaagg cccagccct gatgacaaag 480
 gcagtgggtgc cagaaatgga gaaacgagga ggcggtcag tggatgacgt gtcttcata 540
 gcagccttca gtccatctcc tggcttcagt ccttacaatg tcagtataaac agccttgctg 600
 ggcttcaaca ataccctggc catagagctg gcccgaagga acattagggt gaactgccta 660
 gcacctggac ttatcaagac tagcttcagc aggatgctct ggatggacaa ggaaaaagag 720
 gaaagcatga aagaaaccct gcggataaga aggttaggcg agccagagga ttgtgctggc 780
 atcgtgtctt tcctgtgctc agctacatca ctggggaaac agtgggtgggt 840
 ggtggaggaa ccccgctccc cctctgagga ccggggagaca gccacaggc cagagttggg 900
 ctctagctcc tgggtgctgt cctgcattca cccactggcc tttccacact ctgctcacct 960
 tactgttcac ctcatcaaat cagttctgcc ctgtgaaaag atccagcctt ccctgccgtc 1020
 aaggtggcgt ctactcggg attcctgctg ttgttggggc cttgggtaaa ggcctcccct 1080
 gagaacacag gacaggcctg ctgacaaggc tgagtctacc ttggcaaaaga ccaagatatt 1140
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gcttatgaac	gtcagtatga	acagcaaacc	tatcagggtga	tccctgaggt	gatcaaaaac	180
ttcatccagt	atctccacaa	aactgtctca	gatttgattg	accagaaagt	gtatgagcta	240
caggccagtc	gtgtctccag	tgatgtcatt	gaccagaagg	tgtatgagat	ccaggacatc	300
tatgagaaca	gctggacca	gctgactgaa	agattcttca	agaatacacc	ttggcccag	360
gctgaagcca	ttgtctccaca	ggttggcaat	gatgctgtct	tcctgatttt	atacaaagaa	420
ttatactaca	ggcacatata	tgccaaagtc	agtgggggac	cttccttgga	gcagagggtt	480
gaatcctatt	acaactactg	caatctcttc	aactacattc	ttaatgccga	tggtcctgct	540
ccccttgaac	tacccaacca	gtggctctgg	gatattatcg	atgagttcat	ctaccagttt	600
cagtcattca	gtcagtagcg	ctgtaagact	gccaagaagt	cagaggagga	gattgacctt	660
cttcgttcca	atcccaaaat	ctggaatgtt	catagtgtcc	tcaatgtcct	tcattccctg	720
gtagacaaat	ccaacatcaa	ccgacagttg	gaggtatata	caagcggagg	tgacctgag	780
agtgtggctg	gggagtatgg	gcggcactcc	ctctacaaaa	tgcttggtta	cttcagcctg	840
gtcgggcttc	tccgcctgca	ctccctgtta	ggagattact	accaggccat	caaggtgctg	900
gagaacatcg	aactgaacaa	gaagagtatg	tattcccgtg	tgccagagtg	ccaggtcacc	960
acatactatt	atggttgggtt	tgcatatttg	atgatgcgtc	gttaccagga	tgccatccgg	1020
gtcttcgcca	acatcctcct	ctacatccag	aggaccaaga	gcatgttcca	gaggaccacg	1080
tacaagtatg	agatgattaa	caagcagaat	gagcagatgc	atgcgctgct	ggccattgcc	1140
ctcacgatgt	accccatgcg	tatcgatgag	agcattcacc	tccagctgcg	ggagaaatat	1200
ggggacaaga	tggtgcgcat	gcagaaaggt	gaccacaaag	tctatgaaga	acttttcagt	1260
tactcctgcc	ccaagttcct	gtcgctgtga	gtgcccact	atgataatgt	gcaccccaac	1320
taccacaaag	agcccttcct	gcagcagctg	aaggtgtttt	ctgatgaagt	acagcagcag	1380
gcccagcttt	caaccatccg	cagcttcctg	aagctctaca	ccaccatgcc	tgtggccaag	1440
ctggctggct	tcctggacct	cacagagcag	gagttccgga	tccagcttct	tgtcttcaaa	1500
cacaagatga	agaacctcgt	gtggaccagc	ggtatctcag	ccctggatgg	tgaatttcag	1560
tcagcctcag	aggttgactt	ctacattgat	aaggacatga	tccacatcgc	ggacaccaag	1620
gtcgccaggc	gttatggga	ttcttcac	cgtcagatcc	acaaatttga	ggagcttaat	1680
cgaaccttga	agaagatggg	acagagacct	tgatgatatt	cacacacatt	caggaacctg	1740
ttttgatgta	ttataggcag	gaagtgtttt	tgctaccgtg	aaacctttac	ctagatcagc	1800
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 <212> PRT
 <213> HOMO SAPIENS

<300>

<308> g1079566

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Ala	Arg	Leu	Ser	Val	Arg	Met	Ser	Ser	Thr	Gly	Ile	Asp	Arg	Lys	Gly
			20					25					30		
Val	Leu	Ala	Asn	Arg	Val	Ala	Val	Val	Thr	Gly	Ser	Thr	Ser	Gly	Ile
			35				40					45			
Gly	Phe	Ala	Ile	Ala	Arg	Arg	Leu	Ala	Arg	Asp	Gly	Ala	His	Val	Val
			50			55				60					
Ile	Ser	Ser	Arg	Lys	Gln	Gln	Asn	Val	Asp	Arg	Ala	Met	Ala	Lys	Leu
65					70				75					80	
Gln	Gly	Glu	Gly	Leu	Ser	Val	Ala	Gly	Ile	Val	Cys	His	Val	Gly	Lys
				85					90					95	

Ala Glu Asp Arg Glu Gln Leu Val Ala Lys Ala Leu Glu His Cys Gly
 100 105 110
 Gly Val Asp Phe Leu Val Cys Ser Ala Gly Val Asn Pro Leu Val Gly
 115 120 125
 Ser Thr Leu Gly Thr Ser Glu Gln Ile Trp Asp Lys Ile Leu Ser Val
 130 135 140
 Asn Val Lys Ser Pro Ala Leu Leu Leu Ser Gln Leu Leu Pro Tyr Met
 145 150 155 160
 Glu Asn Arg Arg Gly Ala Val Ile Leu Val Ser Ser Ile Ala Ala Tyr
 165 170 175
 Asn Pro Val Val Ala Leu Gly Val Tyr Asn Val Ser Lys Thr Ala Leu
 180 185 190
 Leu Gly Leu Thr Arg Thr Leu Ala Leu Glu Leu Ala Pro Lys Asp Ile
 195 200 205
 Arg Val Asn Cys Val Val Pro Gly Ile Ile Lys Thr Asp Phe Ser Lys
 210 215 220
 Val Phe His Gly Asn Glu Ser Leu Trp Lys Asn Phe Lys Glu His His
 225 230 235 240
 Gln Leu Gln Arg Ile Gly Glu Ser Glu Asp Cys Ala Gly Ile Val Ser
 245 250 255
 Phe Leu Cys Ser Pro Asp Ala Ser Tyr Val Asn Gly Glu Asn Ile Ala
 260 265 270
 Val Ala Gly Tyr Ser Thr Arg Leu
 275 280

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 <212> PRT
 <213> CAENORHABDITIS ELEGANS

<300>
 <308> g2731377

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 Glu Val Ala Asp Tyr Leu Val Tyr Phe Ser Arg Met Val Asp Glu Gln
 35 40 45
 Asn Val Pro Glu Ile Leu Thr Leu Tyr Asp Gln Ala Phe Pro Asp Leu
 50 55 60
 Thr Glu Arg Phe Phe Arg Asp Arg Met Trp Pro Asp Glu Asn Val Val
 65 70 75 80
 Glu Arg Ile Ile Gly Pro Gly Asn Lys Leu Phe Ile Ile Leu Tyr Lys
 85 90 95
 Glu Leu Tyr Tyr Arg Gln Leu Tyr Ala Arg Asn Thr Arg Gly Pro Leu
 100 105 110
 Leu Val His Arg Tyr Glu Ser Phe Met Asn Tyr Gln Glu Leu Phe Ser
 115 120 125
 Glu Leu Leu Ser Ser Lys Asp Pro Ile Pro Leu Ser Leu Pro Asn Val
 130 135 140
 Trp Leu Trp Asp Ile Ile Asp Glu Phe Val Tyr Gln Phe Gln Ala Phe
 145 150 155 160
 Cys Leu Tyr Lys Ala Asn Pro Gly Lys Arg Asn Ala Asp Glu Val Glu
 165 170 175
 Asp Leu Ile Asn Ile Glu Glu Asn Gln Asn Ala Trp Asn Ile Tyr Pro
 180 185 190
 Val Leu Asn Ile Leu Tyr Ser Leu Leu Ser Lys Ser Gln Ile Val Glu
 195 200 205
 Gln Leu Lys Ala Leu Lys Glu Lys Arg Asn Pro Asp Ser Val Ala Asp
 210 215 220
 Glu Phe Gly Gln Ser Asp Leu Tyr Phe Lys Leu Gly Tyr Phe Ala Leu
 225 230 235 240
 Ile Gly Leu Leu Arg Thr His Val Leu Leu Gly Asp Tyr His Gln Ala

245 250 255
 Leu Lys Thr Val Gln Tyr Val Asp Ile Asp Pro Lys Gly Ile Tyr Asn
 260 265 270
 Thr Val Pro Thr Cys Leu Val Thr Leu His Tyr Phe Val Gly Phe Ser
 275 280 285
 His Leu Met Met Arg Asn Tyr Gly Glu Ala Thr Lys Met Phe Val Asn
 290 295 300
 Cys Leu Leu Tyr Ile Gln Arg Thr Lys Ser Val Gln Asn Gln Gln Pro
 305 310 315 320
 Ser Lys Lys Asn Phe Gln Tyr Asp Val Ile Gly Lys Thr Trp Asp Gln
 325 330 335
 Leu Phe His Leu Leu Ala Ile Cys Leu Ala Ile Gln Pro Gln Arg Ile
 340 345 350
 Asp Glu Ser Ile Ala Ser Gln Leu Ser Glu Arg Cys Gly Glu Arg Met
 355 360 365
 Met His Met Ala Asn Gly Asn Ile Asp Glu Phe Arg Asn Ala Phe Ala
 370 375 380
 Thr Gly Cys Pro Lys Phe Leu Ser Pro Thr Thr Val Val Tyr Glu Gly
 385 390 395 400
 Val Asn Gln Ser Lys Glu Pro Leu Leu Arg Gln Thr Gln Ser Phe Leu
 405 410 415
 Glu Gly Ile Glu Ser Gln Met Ala Leu Pro Val Leu Arg Gly Tyr Leu
 420 425 430
 Lys Leu Tyr Thr Thr Leu Pro Thr Lys Lys Leu Ala Ser Phe Met Asp
 435 440 445
 Val Asp Asp Glu His Tyr Asp Ser Phe Ile Gly Lys Leu Leu Thr Tyr
 450 455 460
 Lys Met Ile Val Asn Glu Leu Gly Lys Glu Ala Gly Pro Ser Ser Ala
 465 470 475 480
 Asp Asp Asp Glu Pro Gln Thr Asp Ile Asp Phe Tyr Val Asp Arg Asp
 485 490 495
 Met Ile Asn Ile Ala Asp Thr Lys Val Ala Arg His Val Gly Cys Ala
 500 505 510
 Gln Thr Thr Arg Tyr Pro Glu Thr Met Ile Leu Lys Lys Phe Val
 515 520 525
 Gly Arg Thr Val Leu Ile Thr Gly Ala Ser Arg Gly Ile Gly Lys Glu
 530 535 540
 Ile Ala Leu Lys Leu Ala Lys Asp Gly Ala Asn Ile Val Val Ala Ala
 545 550 555 560
 Lys Thr Ala Thr Ala His Pro Lys Leu Pro Gly Thr Ile Tyr Ser Ala
 565 570 575
 Ala Glu Glu Ile Glu Lys Ala Gly Gly Lys Ala Leu Pro Cys Ile Val
 580 585 590
 Asp Val Arg Asp Glu Ala Ser Val Lys Ala Ser Val Glu Glu Ala Val
 595 600 605
 Lys Lys Phe Gly Gly Ile Asp Ile Leu Ile Asn Asn Ala Ser Ala Ile
 610 615 620
 Ser Leu Thr Asp Thr Glu Asn Thr Glu Met Lys Arg Tyr Asp Leu Met
 625 630 635 640
 His Ser Ile Asn Thr Arg Gly Thr Phe Leu Met Thr Lys Thr Cys Leu
 645 650 655
 Pro Tyr Leu Lys Ser Gly Lys Asn Pro His Val Leu Asn Ile Ser Pro
 660 665 670
 Pro Leu Leu Met Glu Thr Arg Trp Phe Ala Asn His Val Ala Tyr Thr
 675 680 685
 Met Ala Lys Tyr Gly Met Ser Met Cys Val Leu Gly Gln His Glu Glu
 690 695 700
 Phe Arg Pro His Gly Ile Ala Val Asn Ala Leu Trp Pro Leu Thr Ala
 705 710 715 720
 Ile Trp Thr Ala Ala Met Glu Met Leu Ser Asp Lys Gly Gly Glu Ala
 725 730 735
 Gly Ser Arg Lys Pro Ser Ile Met Ala Asp Ala Ala Tyr Ala Val Leu
 740 745 750
 Ser Lys Asn Ser Lys Asp Phe Thr Gly Asn Phe Cys Ile Asp Glu Asp
 755 760 765

Ile	Leu	Lys	Ala	Glu	Gly	Val	Thr	Asp	Phe	Asp	Arg	Tyr	Ala	Cys	Val
770						775					780				
Pro	Asp	Ala	Pro	Leu	Met	Pro	Asp	Phe	Phe	Ile	Pro	Ala	Gly	Thr	Tyr
785					790					795					800
Asp	His	Lys	Phe	Ser	Ser	Gly	Ala	Gln	Ile	Gly	Lys	Lys	Asn	Lys	Thr
				805					810					815	
His	Glu	Ala	Gly	Val	Val	Glu	Glu	Glu	Ile	Lys	Gln	Ile	Phe	Thr	Ser
			820					825					830		
Ala	Lys	Arg	Leu	Leu	Asn	Ala	Asp	Ile	Val	Lys	Lys	Thr	Gly	Phe	Val
		835					840					845			
Tyr	Glu	Phe	Leu	Leu	Lys	Asp	Pro	Thr	Thr	Lys	Ser	Glu	Arg	Ile	Ile
850						855					860				
Thr	Leu	Asp	Leu	Lys	Asn	Gly	Glu	Gly	Ala	Leu	Thr	Asp	Lys	Lys	Ala
865					870					875					880
Ser	Gly	Lys	Ala	Asp	Val	Lys	Phe	Thr	Leu	Ala	Pro	Glu	His	Phe	Ala
				885					890					895	
Pro	Leu	Phe	Thr	Gly	Lys	Leu	Arg	Pro	Thr	Thr	Ala	Leu	Met	Thr	Lys
			900					905					910		
Lys	Leu	Gln	Ile	Ser	Gly	Asp	Met	Pro	Gly	Ala	Met	Lys	Leu	Glu	Ser
		915				920						925			
Leu	Leu	Arg	Lys	Phe	Thr	Glu	Gly	Lys	Leu						
930						935									